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#2
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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/087,167

DATE: 03/22/2002
 TIME: 10:47:24

Input Set : A:\PTO.VSK.txt
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3 <110> APPLICANT: Pascal, Erica
 4 Valentine, Scott
 5 Brown, Jeffrey
 6 Cockrell, Adam
 7 Johnson, Brian
 9 <120> TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
 11 <130> FILE REFERENCE: 50018A
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/087,167
 C--> 13 <141> CURRENT FILING DATE: 2002-03-01
 13 <150> PRIOR APPLICATION NUMBER: US 60/242,969
 14 <151> PRIOR FILING DATE: 2000-10-24
 16 <160> NUMBER OF SEQ ID NOS: 148
 18 <170> SOFTWARE: PatentIn version 3.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 2840
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Manduca sexta
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (361)..(2031)
 28 <223> OTHER INFORMATION: Manduca sexta Ecdysone Receptor
 31 <300> PUBLICATION INFORMATION:
 32 <301> AUTHORS: Fujiwara, et al.
 33 <302> TITLE: Cloning of an ecdysone receptor homolog from Manduca sexta and the
 34 developmental profile of its mRNA in wings
 35 <303> JOURNAL: Insect Biochem. Mol. Biol.
 36 <304> VOLUME: 25
 37 <305> ISSUE: 7
 38 <306> PAGES: 845-856
 39 <307> DATE: 1995
 40 <308> DATABASE ACCESSION NO: Genbank/U19812
 41 <309> DATABASE ENTRY DATE: 1996-02-03
 43 <400> SEQUENCE: 1
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 48 cttcgattt tggtgtact gaaaagcgcac gcgtatcggt gtcgaagatt ctctataagt 180
 50 gcataatata ttccgagacag tgatagcga ttccgttcgg tttcatcgcc cggatgagtg 240
 52 gttcatgccc gtagagacgc gtttagatag ttatggcgg gaaaaagtga agtggaaagcc 300
 54 tacgtcagag gatgtccctc ggtggtcacg gaagccgggg cgtgtgacgc gctcttcgac 360
 56 atg aga cgc cgc tgg tca aac aac gga tgt ttc cct ctg cga atg ttt 408
 57 Met Arg Arg Arg Trp Ser Asn Asn Gly Cys Phe Pro Ile Arg Met Phe
 58 1 5 10 15
 60 gag gag agc tcc tct gaa gtg act tct tcc tcg gcg ttc ggg atg ccg 456

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61	Glu	Glu	Ser	Ser	Ser	Glu	Val	Thr	Ser	Ser	Ser	Ala	Phe	Gly	Met	Pro
62				20					25					30		
64	gcg	gcc	atg	gta	atg	tca	ccg	gag	tcg	ctg	gcg	tcg	cca	gag	tac	ggc
65	Ala	Ala	Met	Val	Met	Ser	Pro	Glu	Ser	Leu	Ala	Ser	Pro	Glu	Tyr	Gly
66					35				40				45			
68	ggc	ctc	gag	ctc	tgg	agc	tac	gat	gag	acc	atg	aca	aac	tat	ccg	gcg
69	Gly	Leu	Glu	Leu	Trp	Ser	Tyr	Asp	Glu	Thr	Met	Thr	Asn	Tyr	Pro	Ala
70					50				55			60				
72	cag	tca	ctg	ctc	ggc	gcg	tgt	aat	gcg	ccg	cag	cag	cag	caa	cag	
73	Gln	Ser	Leu	Leu	Gly	Ala	Cys	Asn	Ala	Pro	Gln	Gln	Gln	Gln	Gln	Gln
74	65				70				75			80				
76	caa	caa	cag	cag	ccg	tcc	gct	cag	ccg	ctg	tct	atg	ccg	ctg	ccg	
77	Gln	Gln	Gln	Pro	Ser	Ala	Gln	Pro	Leu	Pro	Ser	Met	Pro	Leu	Pro	
78					85				90			95				
80	atg	cct	cct	aca	act	cct	aaa	tca	gag	aac	gag	tcc	atg	tcg	tca	ggt
81	Met	Pro	Pro	Thr	Thr	Pro	Lys	Ser	Glu	Asn	Glu	Ser	Met	Ser	Ser	Gly
82					100				105			110				
84	cga	gaa	gaa	tta	tca	ccg	gcc	tca	agt	ata	aat	gga	tgt	agt	act	gat
85	Arg	Glu	Glu	Leu	Ser	Pro	Ala	Ser	Ser	Ile	Asn	Gly	Cys	Ser	Thr	Asp
86					115				120			125				
88	ggg	gaa	cca	aga	cga	cag	aag	aaa	ggg	cca	gcg	ccg	cgc	cag	cag	gag
89	Gly	Glu	Pro	Arg	Arg	Gln	Lys	Lys	Gly	Pro	Ala	Pro	Arg	Gln	Gln	Glu
90					130				135			140				
92	gaa	ctg	tgc	ctt	gtt	tgc	ggc	gac	agg	gct	tcg	gga	tat	cac	tat	aac
93	Glu	Leu	Cys	Leu	Val	Cys	Gly	Asp	Arg	Ala	Ser	Gly	Tyr	His	Tyr	Asn
94	145				150				155			160				
96	gcg	ctt	acg	tgc	gaa	gga	tgt	aaa	ggg	ttc	ttc	agg	cg	agt	gtg	acc
97	Ala	Leu	Thr	Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe	Arg	Arg	Ser	Val	Thr
98					165				170			175				
100	aag	aat	gcg	gta	tat	att	tgt	aaa	ttt	gga	cac	gcc	tgc	gag	atg	gac
101	Lys	Asn	Ala	Val	Tyr	Ile	Cys	Lys	Phe	Gly	His	Ala	Cys	Glu	Met	Asp
102					180				185			190				
104	atg	tac	atg	agg	aga	aaa	tgc	caa	gag	tgt	cgg	ttg	aag	aaa	tgc	ctc
105	Met	Tyr	Met	Arg	Arg	Lys	Cys	Gln	Glu	Cys	Arg	Leu	Lys	Lys	Cys	Leu
106					195				200			205				
108	gcg	gtg	ggc	atg	agg	ccc	gag	tgc	gtc	gtc	cca	gag	tcc	acg	tgc	aag
109	Ala	Val	Gly	Met	Arg	Pro	Glu	Cys	Val	Val	Pro	Glu	Ser	Thr	Cys	Lys
110					210				215			220				
112	aac	aaa	aga	aga	gaa	aag	gaa	gca	cag	aga	gaa	aaa	gac	aaa	ctg	cca
113	Asn	Lys	Arg	Arg	Glu	Lys	Glu	Ala	Gln	Arg	Glu	Lys	Asp	Lys	Leu	Pro
114	225				230				235			240				
116	gtc	agt	acg	acg	aca	gtg	gac	gat	cat	atg	cct	gcc	ata	atg	caa	tgt
117	Val	Ser	Thr	Thr	Thr	Val	Asp	Asp	His	Met	Pro	Ala	Ile	Met	Gln	Cys
118					245				250			255				
120	gac	cct	ccg	ccc	cca	gag	gcg	gca	agg	att	cac	gaa	gtg	gtc	ccg	agg
121	Asp	Pro	Pro	Pro	Glu	Ala	Ala	Arg	Ile	His	Glu	Val	Val	Pro	Arg	
122					260				265			270				
124	tcc	cta	acg	gag	aag	cta	atg	gag	cag	aac	aga	ctg	aag	aat	gtg	acg
125	Phe	Leu	Thr	Glu	Lys	Leu	Met	Glu	Gln	Asn	Arg	Leu	Lys	Asn	Val	Thr

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128	ccg ctg tcg gcg aac cag aag tcc ctg atc gcg agg ctc gtg tgg tac			1272
129	Pro Leu Ser Ala Asn Gln Lys Ser Leu Ile Ala Arg Leu Val Trp Tyr			
130	290	295	300	
132	cag gag ggg tac gag cag ccg tcg gag gaa gat ctc aag aga gtt aca			1320
133	Gln Glu Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Lys Arg Val Thr			
134	305	310	315	320
136	cag aca tgg cag tta gaa gaa gaa gag gag gaa act gac atg ccc			1368
137	Gln Thr Trp Gln Leu Glu Glu Glu Glu Thr Asp Met Pro			
138	325	330	335	
140	tcc cgt cag atc aca gag atg acg atc tta aca gtg cag ctt att gta			1416
141	Phe Arg Gln Ile Thr Glu Met Thr Ile Leu Thr Val Gln Leu Ile Val			
142	340	345	350	
144	gaa ttc gca aag gga cta ccg gga ttc tcc aag ata tct cag tcc gat			1464
145	Glu Phe Ala Lys Gly Leu Pro Gly Phe Ser Lys Ile Ser Gln Ser Asp			
146	355	360	365	
148	caa att aca tta tta aag gcg tca tca agc gaa gtg atg atg ctg cga			1512
149	Gln Ile Thr Leu Leu Lys Ala Ser Ser Ser Glu Val Met Met Leu Arg			
150	370	375	380	
152	gtg gcg cga cgg tac gac gcg gcg acg gac agc gtg ctg ttc gcg aac			1560
153	Val Ala Arg Arg Tyr Asp Ala Ala Thr Asp Ser Val Leu Phe Ala Asn			
154	385	390	395	400
156	aac cag gcg tac acg cgc gac aac tac cgc aag gcg ggc atg tcc tac			1608
157	Asn Gln Ala Tyr Thr Arg Asp Asn Tyr Arg Lys Ala Gly Met Ser Tyr			
158	405	410	415	
160	gtc atc gag gac ctg ctg cac ttc tgt cgg tgt atg tac tcc atg agc			1656
161	Val Ile Glu Asp Leu Leu His Phe Cys Arg Cys Met Tyr Ser Met Ser			
162	420	425	430	
164	atg gac aat gtg cac tac gcg ctg ctc acc gcc atc gtt ata ttc tca			1704
165	Met Asp Asn Val His Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser			
166	435	440	445	
168	gac cgg cca ggc ctc gag caa ccc ctt tta gtg gag gaa atc cag aga			1752
169	Asp Arg Pro Gly Leu Glu Gln Pro Leu Leu Val Glu Glu Ile Gln Arg			
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172	tac tac ttg aag acg ctg cgg gtt tac att tta aat cag cac agc gcg			1800.
173	Tyr Tyr Leu Lys Thr Leu Arg Val Tyr Ile Leu Asn Gln His Ser Ala			
174	465	470	475	480
176	tcg cct cgc tgc gcc gtg ctg ttc ggc aag atc ctc ggc gtg ctg acg			1848
177	Ser Pro Arg Cys Ala Val Leu Phe Gly Lys Ile Leu Gly Val Leu Thr			
178	485	490	495	
180	gaa ctg cgc acg ctc ggc acg cag aac tcc aac atg tgc atc tcg ctg			1896
181	Glu Leu Arg Thr Leu Gly Thr Gln Asn Ser Asn Met Cys Ile Ser Leu			
182	500	505	510	
184	aag ctg aag aac agg aaa ctt ccg cca ttc ctc gag gag atc tgg gac			1944
185	Lys Leu Lys Asn Arg Lys Leu Pro Pro Phe Leu Glu Glu Ile Trp Asp			
186	515	520	525	
188	gtg gcc gaa gtg tcg acg acg cag ccg acg ccg ggg gtg gcg gcg cag			1992
189	Val Ala Glu Val Ser Thr Thr Gln Pro Thr Pro Gly Val Ala Ala Gln			
190	530	535	540	

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192	gtg acc ccc atc gtg gtg gac aac ccc gcg gcg ctc tag	ctggcgcc	2041	
193	Val Thr Pro Ile Val Val Asp Asn Pro Ala Ala Leu			
194	545	550	555	
196	ggcgccgcgc cccggccccc ccgcccgcgc cgctccccc	cgccgcgcgc	2101	
198	gcggcctgcg ctgagtgcgg gaccgcgc	gaggagagaa	2161	
200	ttagtgaagt gcacggacgc gatcgtggga	ccgcatcgac	2221	
202	aatattaccc cttagggccgg ttegtacgtg	tccgtgacc	2281	
204	gattagtcaa tatatgtgtt gttgaacgtt	tggagagat	2341	
206	agcgcgcggc cggcgcgtgt	cggcagactg	2401	
208	gttttttcg tttgcgaccg	gaaaccgag	2461	
210	cggtcaactcg	gatacgcccg	2521	
212	taaataagtt cacctgtatt	gcgcgtacat	2581	
214	aagtaatata tgaagagatg	acgagaatta	2641	
216	tttcttcga taaataagtt	taaagaaaaaa	2701	
218	ttaactatgtgtt	tttatatttacc	2761	
220	aaaattaact atacgttgat	tgtgctgggt	2821	
222	ggccgacgaa cgcgcgcga	cgttactcg	2840	
225	ccatatttgt ttatata	tttatgtgag		
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240	Ala Ala Met Val Met Ser Pro Glu Ser Leu Ala Ser Pro Glu Tyr Gly			
241	35	40	45	
244	Gly Leu Glu Leu Trp Ser Tyr Asp Glu Thr Met Thr Asn Tyr Pro Ala			
245	50	55	60	
248	Gln Ser Leu Leu Gly Ala Cys Asn Ala Pro Gln Gln Gln Gln Gln			
249	65	70	75	80
252	Gln Gln Gln Pro Ser Ala Gln Pro Leu Pro Ser Met Pro Leu Pro			
253	85	90	95	
256	Met Pro Pro Thr Thr Pro Lys Ser Glu Asn Glu Ser Met Ser Ser Gly			
257	100	105	110	
260	Arg Glu Glu Leu Ser Pro Ala Ser Ser Ile Asn Gly Cys Ser Thr Asp			
261	115	120	125	
264	Gly Glu Pro Arg Arg Gln Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu			
265	130	135	140	
268	Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn			
269	145	150	155	160
272	Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr			
273	165	170	175	
276	Lys Asn Ala Val Tyr Ile Cys Lys Phe Gly His Ala Cys Glu Met Asp			
277	180	185	190	
280	Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu			
281	195	200	205	
284	Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Ser Thr Cys Lys			

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293	245	250	255
296	Asp Pro Pro Pro Glu Ala Ala Arg	Ile His Glu Val Val	Pro Arg
297	260	265	270
300	Phe Leu Thr Glu Lys Leu Met	Glu Gln Asn Arg Leu	Lys Asn Val Thr
301	275	280	285
304	Pro Leu Ser Ala Asn Gln Lys	Ser Leu Ile Ala Arg	Leu Val Trp Tyr
305	290	295	300
308	Gln Glu Gly Tyr Glu Gln Pro Ser	Glu Asp Leu Lys Arg	Val Thr
309	305	310	315
312	Gln Thr Trp Gln Leu Glu Glu Glu	Glu Glu Thr Asp	Met Pro
313	325	330	335
316	Phe Arg Gln Ile Thr Glu Met Thr	Ile Leu Thr Val Gln	Leu Ile Val
317	340	345	350
320	Glu Phe Ala Lys Gly Leu Pro Gly	Phe Ser Lys Ile Ser	Gln Ser Asp
321	355	360	365
324	Gln Ile Thr Leu Leu Lys Ala Ser	Ser Ser Glu Val	Met Met Leu Arg
325	370	375	380
328	Val Ala Arg Arg Tyr Asp Ala Ala Thr Asp	Ser Val Leu Phe	Ala Asn
329	385	390	395
332	Asn Gln Ala Tyr Thr Arg Asp Asn Tyr	Arg Lys Ala Gly	Met Ser Tyr
333	405	410	415
336	Val Ile Glu Asp Leu Leu His Phe	Cys Arg Cys Met	Tyr Ser Met Ser
337	420	425	430
340	Met Asp Asn Val His Tyr Ala	Leu Leu Thr Ala Ile	Val Ile Phe Ser
341	435	440	445
344	Asp Arg Pro Gly Leu Glu Gln Pro	Leu Val Glu Glu	Ile Gln Arg
345	450	455	460
348	Tyr Tyr Leu Lys Thr Leu Arg Val	Tyr Ile Leu Asn Gln	His Ser Ala
349	465	470	475
352	Ser Pro Arg Cys Ala Val Leu Phe	Gly Lys Ile Leu Gly	Val Leu Thr
353	485	490	495
356	Glu Leu Arg Thr Leu Gly Thr Gln	Asn Ser Asn Met Cys	Ile Ser Leu
357	500	505	510
360	Lys Leu Lys Asn Arg Lys Leu Pro	Pro Phe Leu Glu Glu	Ile Trp Asp
361	515	520	525
364	Val Ala Glu Val Ser Thr Thr Gln	Pro Thr Pro Gly	Val Ala Ala Gln
365	530	535	540
368	Val Thr Pro Ile Val Val Asp	Asn Pro Ala Ala	Leu
369	545	550	555
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VERIFICATION SUMMARY
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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
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